

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: August 19, 2004, 23:34:06 ; Search time 99 Seconds
(without alignments)
2152.537 Million cell updates/sec
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Perfect score: 2015
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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -NORM=ext -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1927	95.6	1533	4	US-09-205-258-90
3	1587.5	78.8	1149	4	US-09-970-516-5
4	856.5	42.5	1857	4	US-09-970-516-3
5	198	9.8	2462	4	US-09-620-312D-796
6	147.5	7.3	915	4	US-09-134-000C-1961
7	130	6.5	978	4	US-09-107-532A-3132
8	127.5	6.3	4403765	3	US-09-103-840A-2
9	126.5	6.3	4411529	3	US-09-103-840A-1
10	125.5	6.2	894	4	US-09-134-000C-211
11	118.5	5.9	942	4	US-09-107-532A-3500
12	113	5.6	900	4	US-08-961-527-332

13	113	5.6	1035	4	US-09-134-000C-408	Sequence 408, Ap
14	110	5.5	1003	4	US-09-221-017B-1064	Sequence 1064, Ap
15	108	5.4	13542	4	US-08-956-171E-154	Sequence 154, Ap
16	106.5	5.3	1458	4	US-09-252-991A-14865	Sequence 14865, A
17	105	5.2	975	4	US-09-134-001C-1937	Sequence 1937, Ap
18	103.5	5.1	912	4	US-09-107-532A-1479	Sequence 1479, Ap
19	102.5	5.1	5092	3	US-09-412-545-1	Sequence 1, Appli
20	101	5.0	1548	4	US-09-252-991A-5880	Sequence 5880, Ap
21	99.5	4.9	2493	4	US-09-252-991A-12390	Sequence 12390, A
22	99.5	4.9	3024	4	US-09-252-991A-12202	Sequence 12202, A
23	99.5	4.9	111282	4	US-09-754-250-3	Sequence 3, Appli
24	98	4.9	22481	4	US-08-367-841A-43	Sequence 43, Appl
25	98	4.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl
26	98	4.9	22484	4	US-09-875-223-2	Sequence 2, Appli
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28	98	4.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
29	98	4.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
30	97	4.8	1131	4	US-09-252-991A-691	Sequence 691, Ap
31	97	4.8	3054	4	US-09-252-991A-720	Sequence 720, Ap
32	97	4.8	6885	4	US-09-252-991A-660	Sequence 660, Ap
33	96.5	4.8	5727	4	US-08-956-171E-190	Sequence 190, Ap
34	96	4.8	2657	4	US-09-495-050A-191	Sequence 191, Ap
35	96	4.8	23673	4	US-09-773-816-1	Sequence 1, Appli
36	95	4.7	1800	4	US-09-252-991A-12496	Sequence 12496, A
37	95	4.7	1956	4	US-09-252-991A-9165	Sequence 9165, Ap
38	95	4.7	36519	3	US-08-923-137-2	Sequence 2, Appli
39	94.5	4.7	1851	4	US-09-252-991A-9067	Sequence 9067, Ap
40	94.5	4.7	2849	4	US-09-866-028-77	Sequence 77, Appl
41	94.5	4.7	3681	4	US-09-581-105-1	Sequence 1, Appli
42	94	4.7	1617	4	US-09-252-991A-8802	Sequence 8802, Ap
43	94	4.7	1649	2	US-08-845-566-2	Sequence 2, Appli
44	94	4.7	2416	4	US-09-016-434-1058	Sequence 1058, Ap
45	94	4.7	536165	4	US-09-214-808-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-09-970-516-1

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Query Match:	97.37%	Indels:	0
DB:	4	Gaps:	0

US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

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161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
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RESULT 2
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; Sequence 90, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-05
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
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; EARLIER APPLICATION NUMBER: 60/049,020
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 90
LENGTH: 1533
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1522)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (1527)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-90

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Score: 1927.00 Matches: 371
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Best Local Similarity: 96.36% Mismatches: 11
Query Match: 95.63% Indels: 1
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US-09-784-810C-2 (1-384) x US-09-205-258-90 (1-1533)

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DB 133 CTGAACCCCGCGGGCGGCGAGGCGCTTGCAGCTCTCCCGAGTCACGTGCGGCC 192
QY 41 LeuLeuAlaGluAlaGluSerPheThrLeuMetLeuThrGluArgAsnHisAla 60
DB 193 CTTTGGCTGAGGCTGAATCTCTTCAGCTGATGCTCAGTGGCGGGGACCGCG 252
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DB 313 GACGGCTGATGCACGAGGTGTGAACGGGCTTCATGGAGCGGCTGACTGGGACCGC 372
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DB 433 RAACCATTTATGCTGGCTATRACGAGGTCAACCAATGAACCTCTCTGACCACTGACCGT 492
QY 140 uLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerG1 160
DB 493 ATTGCTGTGCCCGCGCTGTCTACCCATGAACCTGTCTCTGCTGCAACGGCTTCGGG 552
QY 160 YLeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuG1 180
DB 553 GCTGGCCCTCTCTCTGTGTCTGCTGAGCTGGCGGCTTCATTGTGTGTGTGTGTGTGT 612
QY 180 uSerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgIue 200
DB 613 GAGTGAGAAGTATCGGCTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCTCTGCTGT 672
QY 200 uAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPh 220
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QY 240 oLeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVa 260
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QY 300 uArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVa 320
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QY 340 lAspGlyGluLeuMetValSerGluAlaValGlnGlyValHisProAsnTyrPheTr 360
DB 1093 GGATGGGGAATTGATGTTAGCGAGGCGCTGCGAGGCGCAGGTGCACCAAACTACTTCTG 1152
QY 360 pMetValSerGlyCysValGluProProSerTrpLysProGlnGlnMetProProPr 380
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QY 380 oGluGluProLeu 384
DB 1213 AGAAGAGCCCTTA 1225
RESULT 3
US-09-784-810C-2
Sequence 5, Application US/09970516
Patent No. 6610534
GENERAL INFORMATION:
APPLICANT: No. 6610534artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04


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QY 187 LeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaLeuArgThrTyr 206
Db 478 TTAGAAACCTCGCTTATTTATTTTCAGGTGCCAAACATTTAGCGAATGCTCAACGAT 537
QY 207 ArgGlyArgLeu-----AlaThrLeuProVal 215
Db 538 CCTTTTCATTAACTGGATGCAAAAGAACAAACCATTTGAAAGTAGTACCGTTTGTAGTT 597
QY 216 GlyArgVal-----GlyPheLysThrProAlaSerProValValValGlnGln 231
Db 598 GGCCTTAACGATTCAATCGTGGGTTTGAAACATTTATACCAGAGGCCCAAGTGGATGAT 657
QY 232 GlyProValAlaHisLeuValProLeuGluGlnValProSerHisTyr----- 249
Db 658 GGCATAACTT-----CATTTAGTTTATTTAAAGATCAA-----TCATTATGGGATGCA 705
QY 250 ---GlnValValProAsp 254
Db 706 GTAAAGACGATCCAGAT 723

RESULT 7
US-09-107-532A-3132
; Sequence 3132, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...978
; SEQUENCE DESCRIPTION: SEQ ID NO: 3132:
US-09-107-532A-3132

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Alignment Scores:
Pred. No.: 2,32e-05 Length: 978
Score: 130.00 Matches: 51
Percent Similarity: 40.52% Conservative: 43
Best Local Similarity: 21.98% Mismatches: 92
Query Match: 6.45% Indels: 46
DB: 4 Gaps: 10

US-09-784-810C-2 (1-384) x US-09-107-532A-3132 (1-978)
QY 19 ValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
Db 31 ATATTGATCAATCCATCGGCAGCAGCGAAATGGCTATAAAGTA---GCAGAAAGAATT 87
QY 39 GlnProLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgGln 58
Db 88 TTACCGGTATTAAATAAAGCATATTGACTATACACTTCATTATAGTAATACAAAGA 147
QY 59 HisAlaArgGluLeuValArgSer-----GluGluLeuGlyArgTyr----- 72
Db 148 CACGATGCTGAGATTGCTGAAACTTTGGCAAAAGAACATTTGATTCCTTGGATAGAAGA 207
QY 73 -----AspAlaLeuValValMetSerGlyAspGlyLeuMet 84
Db 208 GAACAGAAACAAATCGATACCTTTCCCTTTTGATCATCGTAGGAGGTACGGCCACTTA 267
QY 85 HisGluValValAsnGlyLeuMetGluArgProAspTyrGluThrAlaIleGlnLysPro 104
Db 268 CATCAGTACTTGATACCTTC-----TATCAGATGGAAGTAGAATCCCA 312
QY 105 LeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAla 124
Db 313 GTTGCTTATATTCAGCAGAGTTCTGAAATGATTTTGTCTCGAGGG-----GCA 360
QY 125 GlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArg 144
Db 361 GGCCTTCCAAAAAATCCCAAAAGGACTT-----CACCTGATTTTACAGCT 408
QY 145 ProValLeuSerProMetAsnLeuLeuSerLeu---HisThrAlaSerGlyLeuArgSer 163
Db 409 CAATCACCAGAAAAAGTCCACATATGCTTATGAAGAAAAATAAGTGAAGAAAAAGGA 468
QY 164 PheSerValLeuSerLeuAlaTyrGlyPhe-----IleAlaAspValAspLeuGlu 180
Db 469 ATAGCTGTTAATAATTCGTTATAGGATTAGATGAGCTATCGTCCATGCGCAAAATCAT 528
QY 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 529 TCTTCCACAAAAAGCGATTGAAC-----AAATACAACTTAGGATCATTTTCGTATTTA 582
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 583 TTCTCTATTCTC-----CGTGCTTTATTC 606

RESULT 8
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2

```

Alignment Scores:		
Pred. NO.:	6.7e-05	894
Score:	125.50	Length:
Percent Similarity:	41.9%	Matches:
Best Local Similarity:	23.42%	Conservative:
Query Match:	6.23%	Mismatches:
D.	4	Indels:
Gaps:		54
D.		10

Alignment Scores:		
Pred. NO.:	6.7e-05	894
Score:	125.50	Length:
Percent Similarity:	41.9%	Matches:
Best Local Similarity:	23.42%	Conservative:
Query Match:	6.23%	Mismatches:
D.	4	Indels:
Gaps:		54
D.		10


```
US-09-784-810C-2 (1-384) x US-09-134-000C-211 (1-894)
QY 42 LeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAlaArg 61
Db 19 CTCAAGCAACAAGAACTAAATATACGGCTCTTTACACTGATTACGCTGGACATGAAAA 78
QY 62 GluLeuValArg-----SerGluGluLeu----- 69
Db 79 GAATTCAGGAGGAACTTCGAAACAACCTTACTTCTTGGCTCTGAAGACTTAGACGTT 138
QY 70 GlyArgTrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValAlaAsn 89
Db 139 TCAACTTTTCCAACTTAGTCTAGTGGTGGCGGCGATGACACTACATATATGTCATTAT 198
QY 90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
Db 199 TCATTACTT-----CCATAGATCAACATT-----CCTTAACTATATTC 243
QY 110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db 244 TGGCGCTCTGGAATGATTTTGCAGGAGGGTGGATTATCAAGAAATATTGATAAGCA 303
QY 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
Db 304 TTGCATCAATCTCCGCGCACAGCA-----CGACCA 333
QY 150 MetAsnLeuLeuSerLeuHisThrAlaSer-----GlyLeuArgSer 163
Db 334 AAGAATTCACAACTTATGTAAGGAGGAGGATTAAGCAAGAAATCGGCTTAGCCACC 393
QY 164 PheSerVal-----LeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db 394 AATAATGTTGGCTTAGGCTTGGATGGCA-----ATCGTGGAAAAACCAACGAA 444
QY 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 445 TCGTCATCAAAAAGCCTTAAT-----AAATTAAGCTTGGCTCGCTTCCTATAT 498
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 499 TCATCA-----ATCATTATGCTTTT 522
QY 221 LysThrProAlaSerProValValGlnGlnGlyProVal-AspAlaHisLeuValPr 240
Db 523 AGACAAAGGCTTCCATTTTAGTTGAATGAATGATGTAACATACACATTTAATCGT 582
QY 240 oLeu 241
Db 583 GCTT 586

RESULT 11
US-09-107-532A-3500
; Sequence 3500, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3500:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 base pairs
TYPE: nucleic acid
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...942
SEQUENCE DESCRIPTION: SEQ ID NO: 3500:
US-09-107-532A-3500
```

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Alignment Scores:
Pred. No.: 0.000476 Length: 942
Score: 118.50 Matches: 53
Percent Similarity: 44.22% Conservative: 58
Best Local Similarity: 21.12% Mismatches: 89
Query Match: 5.88% Indels: 51
DB: 4 Gaps: 10
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US-09-784-810C-2 (1-384) x US-09-107-532A-3500 (1-942)
QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysAlaLeuGlnLeuPheArg 35
Db 64 AAAGTTTTTATTAGTGTAAACCCAGTTTCAGCGGTGAACAAGCA-----AAG 111
QY 36 SerHisValGlnProLeuAlaGluAlaGluIleSerPhe-----ThrLeuMet 52
Db 112 GAATTTGACCAATTAGCGATAGCAAAATTTGAAATCGGTGTTGATGAAGTGTCTCTTG 171
QY 53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrp 72
Db 172 CATACAAAAAAGCAGCGGATGCAAAAACTTTACTCGCAAGCGGCTACGGAAGGGTAT 231
QY 73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAlaAsnGlyLeuMet 92
Db 232 CATAGTGTGTTTTCATCGGCGGAGATGGAACAGTCAACGAAGGAATCAGTGAATCGCT 291
QY 93 Glu-----ArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
Db 292 GAAACAAGAACATCGGCCAAATTTTCGA-----TTTTTCCCA 327
QY 110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db 328 TTGGGTACGGTGAATGACTTGGCTCGAGCATTAGGGATACCGCTAGAACCTTAGGAAGCG 387
QY 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
Db 388 ATCAATCATTTTTCGATTGAATCA-----GTCAAGCA 420
QY 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
Db 421 TTGGATATGGAAAAATAAATATGAC-----GACTATTTATGATGTCGTC 465
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Qy 170 AlaTrpGlyPheIleAlaaspVal-----AspLeuGluSerAspLysTyrArgArgLeu 187
Db 466 GCAATTGGCTCTATCCCTGAATCAATCAATGATGATGATGCGGAGAGACGAAATTT 525
Qy 188 GlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArg 207
Db 526 GGAAAACTAGCTATTATTCATGTCAGGAATCAAAACAGTTAGCTTCACACAACTCTACTCG 585
Qy 208 GlyArgLeu-----AlaThrLeuProValGly 216
Db 586 TTTCACGTAGAGCTGATGAGAAAGAGAGAAATTCAGAGCAGTACCTTGCTGATAGGA 645
Qy 217 ArgVal-----GlyPheLysThrProAlaSerProValValValGlnGlnGly 232
Db 646 CTAACCTAACCTCAGTCGGCGGTTTGAACACATTACTTCCAAATGACCAAGTGGATGATG 705
Qy 233 ProValaspAlaHisLeuValProLeuGluGlu 243
Db 706 AAGCTC-----CATTTGGTTTATTATAAAGAT 732

RESULT 12
US-08-961-527-332/C
; Sequence 332, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Hp Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: FB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-332

Alignment Scores:
Pred. No.: 0.00193 Length: 900
Score: 113.00 Matches: 47
Percent Similarity: 49.39% Conservativeness: 34
Best Local Similarity: 28.66% Mismatches: 54
Query Match: 5.61% Indels: 29
DB: 4 Gaps: 8

US-09-784-810C-2 (1-384) x US-08-961-527-332 (1-900)
Qy 16 ArgValLeuValLeuLeuLeuLeuProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35

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Db 472 AAACCAATGGTAAATATCAACCTACTCTCTGGTGGCGAGAAGGCTTTG----- 425
Qy 36 SerHisValGlnProLeuAlaGluAlaGluLeuSerPheThrLeuMet----- 52
Db 424 GATTACAAAAGAAAAGCTGGAGAAATAAAGCAAAAGAAATACTTTGAATATGTTGAAACCAA 365
Qy 53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTTP 72
Db 364 ATTACCGAAAAGCGCTGGATGCACACATTTTGCTGAAGAAGCTCTCTGTCGACGAGTAT 305
Qy 73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
Db 304 GATCAGTGGTGTGTTGGTGGAGATGGAACGTCTCAATGAAGTCAATTTCCAGTATGAT 245
Qy 93 GluArgProAspTTPGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGlySer 112
Db 244 GAGAGA---GACTAC-----ATTCTTAAG---TTAGGGATTATCCCGCGGTACG 200
Qy 113 GlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnValThrAsnGlu 132
Db 199 GGTAACCTCATTCACAAAACCTTTTGGAA-----ATCAATCAA 164
Qy 133 AspLeu-----LeuThrAsnCysThrLeu-----LeuLeuCysAr 144
Db 163 GACATCGATGGCGCAATTCAGCACTGGATTTGATTTAACCAATGAATGATATCGGT 104
Qy 144 gProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPh 164
Db 103 AAAGCAAAATGACACTATTGTTGGTTATATCTTTAGTATCGGTTCTCTGCTGAGGCGATT 44
Qy 164 eSerValLeu 167
Db 43 CACAATGTTG 34

RESULT 13
US-09-134-000C-408
; Sequence 408, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-408

Alignment Scores:
Pred. No.: 0.00242 Length: 1035
Score: 113.00 Matches: 71
Percent Similarity: 33.14% Conservativeness: 45
Best Local Similarity: 20.29% Mismatches: 132
Query Match: 5.61% Indels: 102
DB: 4 Gaps: 13

US-09-784-810C-2 (1-384) x US-09-134-000C-408 (1-1035)
Qy 19 ValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
Db 34 GTGATTATTAATCAACGTCAGGAAAA-----GAGTTATCAAAAGAACTTA 81
Qy 39 GlnProLeuLeuAla-----GluAlaGluLeuSerPheThrLeu 51
Db 82 CGCGATATTTTATCTATTTTAGAAGATGTTGTTATCAAGCCAGTCATTTGCCACC--- 138

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QY 52 MetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
Db 139 -----ACACGAGAGAAAATTCAGCAGCAATGAAGCAGCATCGTGTGCGCGGCGAGGA 192
QY 72 TrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAsnGly--- 90
Db 193 TTTGATTACTAGTAGCTGCGAGGTGGAGATGGGACCATTATGAAGTCGTAATGGGATT 252
QY 91 -----LeuMetGluArgProAspTyrGluThrAlaIleGlnLysProLeuCysSerLeu 108
Db 253 GCTCCGTGTAAGCGCGCCCT-----AAAATGCTATTATT 288
QY 109 ProAlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGln 128
Db 289 CTTGCTGAGACGAGTACTATGCACGGCCCTTGAG----- 327
QY 129 ValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSer 148
Db 328 -----ATTCTCGTGATAATATCGTTAAGCGCAGCAGAGTGATTAAA 369
QY 149 ProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSer 168
Db 370 AAAAATCAAACTGCAAAATGGATTTGGCCAAAGCGGCAAAATTTACTTTATCAATATT 429
QY 169 LeuAlaTyrGlyPheIleAlaAspValAspLeuGluSerAspLysTyrArgArgLeuGly 188
Db 430 CGCGCGGGTGTTCATTTAACGGAAGTACTTGAAGTTCG----- 471
QY 189 GluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGly 208
Db 472 -----TCAGAGTTGAAAGTATTTTGGT 495
QY 209 ArgLeuAlaThrLeuProValGly-----ArgValGlyPheLysThrPro 223
Db 496 TACTTACGCTACTTAGCCAAAGAGCGCAATGTCGCGGAGTG----- 540
QY 224 AlaSerProValVal-----ValGlnGlnGlyProValAsp 235
Db 541 ---AAGCCGATTAATAATGCGCATGACGTATGATGAAGTGTGTACGAGGCAATGCATCA 597
QY 236 AlaHisLeuValProLeuGluGluGlnValProSerHisTrpGlnValValProAspGlu 255
Db 598 ATGTTTTTCCTAGGGCTGACTAATCGGTGGGTGTTTGGAGCAAAATCGTACCAGAT--- 654
QY 256 AspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAla 275
Db 654 ----- 654
QY 276 ProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSer 295
Db 655 -----GCTAAATTAGACGATGTAAGTTTTCATTTAATCAATGTAAGGCAATATT 708
QY 296 ArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGlu 315
Db 709 TTTGAGATTCTCTATTAGTTGGTGAATGTTAAATGGTGAAGCATGTTGAAGATCAT 768
QY 316 CysProTyrLeuValTyrValProValValAlaPheArgLeuGlu-----ProLysAsp 333
Db 769 -----CGACTGATCTATACAAAGACCAGCTATTATCATGCAGAACGTTAGAAAAGAAC 822
QY 334 GlyLysGlyValPheAlaValAspGlyGlu 343
Db 823 AATAAAATGATGATTAAATTTAGATGGTGAA 852

RESULT 14
US-09-221-017B-1064/c
; Sequence 1064, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 1064:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...1003
US-09-221-017B-1064

Alignment Scores:
Pred. No.: 0.00514 Length: 1003
Score: 110.00 Matches: 82
Percent Similarity: 35.26% Conservative: 58
Best Local Similarity: 20.65% Mismatches: 139
Query Match: 5.46% Indels: 118
DB: 4 Gaps: 19

US-09-784-810C-2 (1-384) x US-09-221-017B-1064 (1-1003)

QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg 35
Db 950 AAGATTCTAGCCATTATCAATNCCATATCGGCGCATCGGATCG-----AAA 906
QY 36 SerHisValGlnProLeuLeuAlaGlu-----AlaGluIleSerPheThrLeuMetLeu 53
Db 905 AGCAACATACCGAGCCTTATAGCCGATGATTTCGCCCATGATCTCAGAACTCTTATC 846
QY 54 Thr-----GluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
Db 845 ACCTATTTCGCAACGTGCTGGCCATCGACGTGAATTGGCAGCAGCAGCAGTGGAGAGCAT 786

```

QY 72 TrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeu 91
DB 785 TAGACATCGCTATTGCGAGTGGAGCGGATGGAACGGTGAACGAGATAGCCCAAGCCTT 726
QY 92 MetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGly 111
DB 725 -----CGCTACACCGATGTAGTGTGGTATCGTCCGGAAGGA 687
QY 112 SerGlyAsnAlaLeuAlaIleSerLeuAsn----- 121
DB 686 TCAGGCAACCGGTGGCGCTGCGCTCCCAAGCTCCCACTCCGCGGAAAGCTCTCGAA 627
QY 122 ---HisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
DB 626 GTGATCAGACCGCGACATGTTCCACCC-----ATCGACTGCTGTGAA 585
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
DB 584 CGGATAGTCCGCTCTTCTTTCCACCTCGCGGATG----- 549
QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
DB 548 -----GGATTTCGATCCGAGCTT----- 531
QY 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
DB 530 AGCAAGAAATTCGCCCAAGCGGTAGTCGA----- 501
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
DB 500 -----GGCCCTATCATCTTAT 486
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHis----- 237
DB 485 CGCGGAACCATGATCGAGAGTTACCTCCAAACGAAGCAAGGATCCAAACTCAGCATAG 426
QY 238 ---LeuValProLeuGlu-GluGlnValProSerHisTyrPheGlnValValProAspGluAs 256
DB 425 ACGCAAAATCCTTTGAGGAGAAAGCTTCTCTCTCAC-----TTGGTGCCA----- 380
QY 256 pPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPheAlaAlaPr 276
DB 379 -----ATGCGCCCGCATGATGCAATAACCGCTTATATCGCTCC 342
QY 276 oMetGlyArgAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly----- 293
DB 341 ATTACGGATTTGGAGGATGTAATAATGGATGTAGTTATTATCCGCTTCAATCCATT 282
QY 294 -ValSerArgAlaMetLeuLeuArgLeuPheLeu---AlaMetGluLysGlyArgHisMe 312
DB 281 GGAAGCTCCCAATGGCTTTTACACTCTTTTACCAAGCGTATCAACAGCAACTCCAATCT 222
QY 312 tGlu---TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluPr 331
DB 221 GGACACCTATAAGCGCCCAAAACCTGATCATT-----CA 189
QY 331 oLysAspGlyLysGlyValPheAlaValAspGlyGlu-LeuMetValSerGluAlaValG 351
DB 188 CGGTGACAGAGGGCGGTAATGACCTTCGATGGGATCTTGTATGTTGGTAAGCGCAT 129
QY 351 lngGlyGlnVal-----HisProAsnTyrPheTrpMetValSerGlyCysValG 367
DB 128 TGAGATCCGCACCTACGCGCGGTCACTCAAGGTATTG---CTACTGAAACCTACACTTG 72
QY 367 luProProProSerTrp---LysProGlnGlnMetProProProGlu 381
DB 71 AAAGTCCCACTCTTTCTAAACCAAAATAAATCCCGTAACCGGAG 25

```

RESULT 15

US-08-956-171E-154/c

; Sequence 154, Application US/08956171E

; Patent No. 6593114

```

; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 154:
; US-08-956-171E-154

Alignment Scores:
Pred. No.: 0.584 Length: 13542
Score: 108.00 Matches: 70
Percent Similarity: 35.52% Conservative: 60
Best Local Similarity: 19.13% Mismatches: 126
Query Match: 5.36% Indels: 110
DB: 4 Gaps: 18

US-09-784-810C-2 (1-384) x US-08-956-171E-154 (1-13542)
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DB 5619 CGTGTAGATCACTTATTATACCCGACATCAGGTAAA-----GAGCTATTATAA 5572
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluLysSerPheThrLeuMetLeuThrGlu 55
DB 5571 -----AGAGAAATTAACCTGATGCTTAAATAAATTAGAA 5539
QY 56 ArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGly----- 70
DB 5538 AAACGGGATATGAACACGAGTGCATATGCAACCGAGAAATAGGTGATGCCACTTGAA 5479
QY 71 -----ArgTrpAspAlaLeuValMetSerGlyAspGlyLeu 83
DB 5478 GCAGAAAGAGCTATGCATGAAATTTATGATGTTATTAATCGTCAGGTGGTGAACA 5419
QY 84 MethisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLys 103

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Db 5418 TTAATGAGTAGTATGTTATCGCAGAAAGCCTAAT-----CGTCCT 5374
Qy 104 ProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyr 123
Db 5373 AAGCTAGGTGTCATCTATGGTACTGTTAATGACTTTGGACGTCGATTCAT-----5320
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Db 5319 -----ATACCTAATGAC-----5308
Qy 144 ArgProValLeuSerProMetAsn---LeuLeuSerLeuHisThrAlaSerGlyLeuArg 162
Db 5307 -----ATCATGGGGCATTGATGTCATCATTTAAGGTCATCTACTATAA-----5263
Qy 163 SerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAsp 182
Db 5262 -----GTAGATATTGGTAAATGAATAAT 5239
Qy 183 LysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAla 202
Db 5238 CGATAC-----TTTATTAAATTTAGCTGCA 5215
Qy 203 LeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThr 222
Db 5214 -----GGCGGACAAATTGACG-----CAAGTCTCTTATGAACA 5182
Qy 223 ProAlaSerProValValGlnGlnValProValAspAlaHisLeuValProLeuGlu 242
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Qy 243 GluGlnValProSer-----HisTrpGlnValVal 252
Db 5127 GAAATGTTACCTCAATCAAAAGCTGTAGATTTAAGAAATTGAATATGATGCTAATGTTTC 5068
Qy 253 ProAspGluAspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMet 272
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Qy 273 PheAlaAlaProMetGlyArgCysAlaAlaGlyValMethHisLeuPheTyrValArgAla 292
Db 5007 TTA---GTGCCGGACGCTAGTTAGATGACGGCTATTTTACGTTTATTATAGTTGAAAAA 4951
Qy 293 GlyValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet 312
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Qy 313 GluTyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLys 332
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Qy 333 AspGlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGly 352
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Qy 353 GlnValHisProAsnTyr 358
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Search completed: August 20, 2004, 01:37:43

Job time : 2820 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 20, 2004, 00:51:17 ; Search time 586 Seconds

(without alignments)

3218.872 Million cell updates/sec

Title: US-09-784-810c-2

Perfect score: 1

Sequence: 1 MDPAGGRGVLPKPCRVLVL.....CVBPSPSKWQMPPEPL 384

Scoring table:

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3228839 seqs, 245606551 residues

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100

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-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

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10: /cgn2_6/ptodata/2/pubpna/us09B_PUBCOMB.seq:*

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12: /cgn2_6/ptodata/2/pubpna/us09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/us10A_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/2/pubpna/us10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/us10E_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/us10F_NEW_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/us10G_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
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ALIGNMENTS

RESULT 1

US-09-784-810A-1

; Sequence 1, Application US/09784810A

; Patent No. US20020082203A1

; GENERAL INFORMATION:

; APPLICANT: RASTELLI, LUCA

; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING

; TITLE OF INVENTION: SAME

; FILE REFERENCE: 10716-08

; CURRENT APPLICATION NUMBER: US/09/784,810A

; PRIOR FILING DATE: 2001-02-14

; PRIOR APPLICATION NUMBER: 60/182,360

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: 60/191,261

; PRIOR FILING DATE: 2000-03-22

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1600

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified_base

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	2	1962	97.4	1152	16	US-10-348-052-22	Sequence 22, Appl
	3	1962	97.4	1152	17	US-10-622-011-22	Sequence 22, Appl
	4	1962	97.4	1155	9	US-09-970-516-1	Sequence 1, Appl
	5	1962	97.4	1155	17	US-10-619-344-1	Sequence 1, Appl
	6	1962	97.4	1799	15	US-10-354-358-25	Sequence 25, Appl
	7	1959	97.2	1205	17	US-10-642-289-1	Sequence 1, Appl
	8	1944	96.5	1562	16	US-10-264-237-1180	Sequence 1180, Ap
c	9	1927	95.6	1533	10	US-09-933-767-90	Sequence 90, Appl
	10	1927	95.6	1533	13	US-10-004-860-90	Sequence 90, Appl
	11	1927	95.6	1533	15	US-10-023-282-90	Sequence 90, Appl
	12	1594.5	79.1	1759	9	US-09-784-810A-3	Sequence 3, Appli
	13	1587.5	78.8	1149	9	US-09-970-516-5	Sequence 5, Appli
	14	1587.5	78.8	1149	17	US-10-619-344-5	Sequence 5, Appli
	15	856.5	43.4	2898	9	US-09-817-678A-11	Sequence 11, Appl
	16	856.5	42.5	1857	9	US-09-970-516-3	Sequence 3, Appli
	17	856.5	42.5	1857	17	US-10-619-344-3	Sequence 3, Appli
	18	856.5	42.5	2380	9	US-09-817-676A-13	Sequence 13, Appl
	19	856.5	42.5	2380	15	US-10-354-358-77	Sequence 77, Appl
	20	856.5	42.5	2380	17	US-10-283-975A-515	Sequence 515, App
	21	550	27.3	2629	16	US-10-348-052-24	Sequence 24, Appl
	22	550	27.3	2629	17	US-10-622-011-24	Sequence 24, Appl
	23	492.5	24.4	2609	16	US-10-348-052-25	Sequence 25, Appl
	24	492.5	24.4	2609	17	US-10-622-011-25	Sequence 25, Appl
	25	481	23.9	480	9	US-09-783-590-9248	Sequence 9248, Ap
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	27	436	21.6	801	13	US-10-296-115-69	Sequence 69, Appl
	28	427	21.2	1869	13	US-10-425-114-34806	Sequence 34806, A
	29	402.5	20.0	1833	17	US-10-437-963-30650	Sequence 30650, A
	30	365	18.1	296	9	US-09-777-564-658	Sequence 658, App
	31	365	18.1	296	15	US-10-015-219-658	Sequence 658, App
	32	363	18.0	1172	17	US-10-283-975A-584	Sequence 584, App
	33	363	17.9	199	9	US-09-796-692-2905	Sequence 2905, Ap
	34	360	17.9	199	15	US-10-040-862-2905	Sequence 2905, Ap
	35	360	17.9	199	16	US-10-057-475B-2905	Sequence 2905, Ap
	36	360	17.9	199	16	US-10-154-884B-2905	Sequence 32, Appl
	37	355.5	17.6	2064	17	US-10-622-011-32	Sequence 58701, A
	38	344.5	17.1	1916	17	US-10-437-963-58701	Sequence 30, Appl
	39	337	16.7	1875	17	US-10-622-011-30	Sequence 20952, A
c	40	305.5	15.2	832	13	US-10-029-386-20952	Sequence 23, Appl
	41	301.5	15.0	1521	13	US-10-168-582-23	Sequence 23, Appl
	42	300	14.9	1394	16	US-10-264-049-204	Sequence 30651, A
	43	295	14.6	422	17	US-10-437-963-30651	Sequence 95148, A
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c	45	275	13.6	507	15	US-10-029-386-7252	

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; LOCATION: (1)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-09-784-810A-1

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Pred. No.: 9,52e-247 Length: 1600
Score: 2015.00 Matches: 384
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-784-810C-2 (1-384) x US-09-784-810A-1 (1-1600)

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Qy 21 LeuAsnProArgGlyGlyLysAlaLeuGlnPheArgSerHisValGlnPro 40
Db 236 CTGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 295
Qy 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgAsnHisAla 60
Db 296 CTTTGGCTGAGGCTGAAATCTCTTTCAGCTGATGCTCACTGAGCGCGCGCGCGCGCGCG 355
Qy 61 ArgGluLeuValArgSerGluLeuGlyValArgTrpAspAlaLeuValValMetSerGly 80
Db 356 CGGAGCTGTGGCTCGGAGGAGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
Db 416 GACGGGCTGATGACGAGGTGGTGAACGGGCTCATGGAGCGGCGCTCACTGGAGACCGGC 475
Qy 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaLeuSerLeu 120
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Qy 121 AsnHisTrpAlaGlyTrpGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
Db 536 AACCATATCTGGCTATGAGCAGGTCACCAATGAAGACCTCTGACCAACTGACGCTA 595
Qy 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db 596 TTGCTGTGCGCGCGCGGCTGTCACCATGAACCTGCTCTGTCACACGCGCTTCGGGG 655
Qy 161 LeuArgSerPheSerValLeuSerLeuAlaTrpPheIleAlaAspValAspLeuGlu 180
Db 656 CTGGCTTCGTTCTCTGCTCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 715
Qy 181 SerAspLysTrpArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 716 AGTGATAAGTATCGCGCTGCGGCGAGATGCGCTTCACTCTGGCGCACTTCTCTGCGCTG 775
Qy 201 AlaAlaLeuArgThrTrpArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
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Qy 241 LeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
Db 896 CTGGAGAGCAGGTCCTTCTCACTGCGAGGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCG 955
Qy 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
Db 956 CTGGCACTGTGCACTCGCACCTGGCGAGTGAGATGTTTGTGCTGACCCATGGCGCGCTGT 1015
Qy 281 AlaAlaGlyValMetHisLeuPheTrpValArgAlaGlyValSerArgAlaMetLeuLeu 300
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RESULT 2
US-10-348-052-22
; Sequence 22, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Eyrst, Henrik
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348,052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-348-052-22

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Score: 1962.00 Matches: 375
Percent Similarity: 98.18% Conservatives: 2
Best Local Similarity: 97.66% Mismatches: 7
Query Match: 97.37% Indels: 0
DB: 16 Gaps: 0

US-09-784-810C-2 (1-384) x US-10-348-052-22 (1-1152)

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; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-10-619-344-1

Alignment Scores:
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Score: 1962.00 Matches: 375
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Query Match: 97.37% Indels: 0
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US-09-784-810C-2 (1-384) x US-10-619-344-1 (1-1155)

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Qy 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
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Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
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Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
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Qy 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
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Qy 201 AlaAlaLeuArgThrTrpArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
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Qy 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
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Db 781 CTGGCACTGCTGCACCTCGACCTGGCAGTGAGATGTTTGTCTGCACCCATGGGCGCTGT 840
Qy 281 AlaAlaGlyValMetHisLeuPheTrpValArgAlaGlyValSerArgAlaMetLeuLeu 300
Db 841 GCAGCTGGCGTCAATGTCATCTGTCTACGTGCGGGGGAGTGTCTCGTGCATGCTGCTG 900
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Qy 321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
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Qy 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTrpPheTrp 360
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Qy 361 MetValSerGlyCysValGluProProSerTrpLysProGlnGlnMetProProPro 380
Db 1081 ATGGTCAGCGTGTGCTGGAGCCCCCGCCAGCTGGAAGCCCGACAGATGCCACGCCA 1140
Qy 381 GluGluProLeu 384
Db 1141 GAAGAGCCCTTA 1152

RESULT 6
US-10-354-358-25
; Sequence 25, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7650, 25641, 69683, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 5252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 26582, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; FILE REFERENCE: MP102-020P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395

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QY 124 AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCys 143
Db 1093 GCTGGTATGAGCAGGTGACCAATGAGACCTCTGACCACTGACGCTATTTGCTGTC 1034
QY 144 ArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSer 163
Db 1033 CGCGGCTGTCTGATCCCATGACCTGCTCTCTGACACAGCTTCGGGGCTGGCCCTC 974
QY 164 PheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAspLys 183
Db 973 TTCTCTGTGCTAGCCCTGGCTGGCTGCTCATTTGCTGATGTGGACCTAGAGATGAGAAG 914
QY 184 TyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaLeu 203
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QY 204 ArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThrPro 223
Db 853 CGCACCTACCGCGCGACTGGCTACCTCCCTGTAGGAAGAGTGGTTCGAAGACACCT 794
QY 224 AlaSerProValValGlnGlnGlnGlyProValAspAlaHisLeuValProLeuGluGlu 243
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Db 733 CCAGTGCCTCTCTACCTGGACAGTGGTGGCGGACGAGGACTTTGTGCTAGTCTGGCAGT 674
QY 264 LeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCysAlaAlaGly 283
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QY 284 ValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeuArgLeuPhe 303
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QY 304 LeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuValTyrValPro 323
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QY 384 Leu 384
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; Sequence 90, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007F2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
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; PRIOR FILING DATE: 1997-12-18
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; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
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; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
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; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
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; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (123)
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; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-933-767-90

Alignment Scores:
Pred. No.: 1.58e-235 Length: 1533
Score: 1927.00 Matches: 371
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Best Local Similarity: 96.36% Mismatches: 11
Query Match: 95.63% Indels: 1
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QY 21 LeuAsnProArgGlyGlyLysAlaLeuGluLeuPheArgSerHisValGlnPro 40
Db 133 CTGAACCCGCGCGCGGCAAGGCAAGGCCCTTCAGCTCTTCGGAGTCACGTGACGCC 192
QY 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgGlnHisAla 60
Db 193 CTTTGGCTGAGCTGAATCTCTTCAGCTGATGCTCACTGAGCGCGGCAACACACGCG 252

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QY 81 AspGlyLeuMetHisGluValValAsnGlyLeu-MetGluArgProAspTrpGluThrAl 100
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QY 100 alieGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLe 120
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QY 120 uAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysPhe 140
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 ; Sequence 90, Application US/10004860
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 ; GENERAL INFORMATION:

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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: SITE
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; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (123)
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; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-023-282-90

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Pred. No.: 158e-235 Length: 1533
Score: 1927.00 Matches: 371
Percent Similarity: 96.88% Conservative: 2
Best Local Similarity: 96.36% Mismatches: 11
Query Match: 95.63% Indels: 1
DB: 15 Gaps: 0

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 ; Patent No. US20020082203A1
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 ; APPLICANT: RASTELDI, LUCA
 ; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
 ; FILE REFERENCE: 10716-08
 ; CURRENT APPLICATION NUMBER: US/09/784,810A
 ; CURRENT FILING DATE: 2001-02-14
 ; PRIOR APPLICATION NUMBER: 60/182,360
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: 60/191,261
 ; PRIOR FILING DATE: 2000-03-22
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 ; SOFTWARE: PatentIn Ver. 2.1
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 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-09-784-810A-3
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 DB: 9 Gaps: 1
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 Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
 Db 507 AGGAGCTGTGTGTGTCAGAGGAGTTCGGTCACTGGGACGCCCTGGCAGTCATGTCCGGT 566
 Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
 Db 567 GATGGTCTGATGATGAATGGTGAATGGCTAATGCAACGGCCAGACTGGAGACTGCC 626
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US-09-784-810C-2 (1-384) x US-10-619-344-5 (1-1149)
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Db 61 CTGAACCCCGAGGTGGCAGGCGCAAGGCTCTGCAGCTCTTCCAGAGCGGTGTGCAGGCC 120
Qy 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgArgHisAla 60
Db 121 TTCTCGAGGAGCGAGAGATAACCTTTAAACTGATACTCACCGAAGCGAAGAACCATGCC 180
Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
Db 181 AGGAGCTGTGTGTGAGAGGAGTTGGGTCACTGGGAGCGCTGGCAGTCAATGTCGGT 240
Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
Db 241 GATGGTCTGATGATGAGTGGTGAATGGCTAATGGAACGGCCGAGCTGGAGAGCTGCC 300
Qy 101 IleGlnLysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
Db 301 ATCCAGAAACCCCTGTGTAGCTCCCTGGAGGCTCCGGCAATGCGTGGCAGCTTCTGG 360
Qy 121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
Db 361 AACCATCTCTGGTACGAGCAGGTGACTTAATGAAGACCTGTCTCATCACTGCACACTG 420
Qy 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
Db 421 CTGTGTGCGCGCGCGCGCTGTCAACCATGAACCTGTCTGCTGCGTGCACACTGCTTGG 480
Qy 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
Db 481 CTGGGCTCTATCTGTGCTCAGTCTGTCTGGGCTTGTGCTGACGCTGGACCTCGAG 540
Qy 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
Db 541 AGTGAGAAGTACAGCGCTTGGGGAGATTCGTTTCACAGTGGGACCTTCTTTCGCCTA 600
Qy 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
Db 601 GCAAGCTCTGGCATCTACCAAGGCGCACTGGCTTCTTCTGTAGAACTGTGGCTCT 660
Qy 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
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Qy 241 LeuGluGlnValProSerHisTyrGlnValValProAspGluAspPheValLeuVal 260
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Qy 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
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RESULT 15
US-09-817-676A-11
; Sequence 11, Application US/09817676A
; Patent No. US20020042101A1
; GENERAL INFORMATION:
; APPLICANT: Kohama, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
; TITLE OF INVENTION: Expression and Methods of Use Thereof
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/194,318
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2698
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (387)..(2237)
; PUBLICATION INFORMATION:
; TITLE: Molecular cloning and functional characterization of a
; JOURNAL: J. Biol. Chem.
; VOLUME: 275
; ISSUE: 26
; PAGES: 19513-19520
; DATE: 2000-06-30
; DATABASE ACCESSION NUMBER: AF245448
; DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-11
Alignment Scores:
Pred. No.: 1,11e-100 Length: 2698
Score: 875.00 Matches: 187
Percent Similarity: 51.98% Conservative: 63
Best Local Similarity: 38.88% Mismatches: 111
Query Match: 43.42% Indels: 120
DB: 9 Gaps: 4
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Qy 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluLeuSerPhe 49
Db 867 GCCTGGCAGCCCTGTATGGACCACGTGGTCCCATGATCTCTGAAGCTGGGCTGCTCTTC 926
Qy 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
Db 927 AACCTCATACAGACAGAACGACAGAACCATGCCGTGAGCTGGTGCAGGGGTTAAGCCTG 986
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Db 987 AGTGAAGTGGGAGGCGATGTGCTGTCTGGAGACGGGCTGCTTTACGAGGTGCTGAT 1046
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Db 1767 TCTTGGGGTTCCTGCTCCACCCAGCAGTCCCGCAGAGCCCTCTACCTGGGGCCCCAGTG 1826
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Db 1887 GAG---TTTGTACTCATGTTGGCACTTGACAGAGCCCTCTGCCGACGACCTGATGGCA 1943
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